

---

(05-1-105)

## Launching functional study of Chinese cabbage genes, whose function is not known, in *Arabidopsis*

**Jongsoon Kim, Sang-Il Kwak, Dong-pyo Seo, Yeon-Hee, Lee<sup>1</sup>, Yoonkang Hur\***

Department of Biology, School of Biosciences and Biotechnology, Chungnam National University, Daejeon 305-764, Korea

<sup>1</sup>National Institute of Agricultural Biotechnology (NIAB), Rural Development Administration, Suwon 441-707, Korea.

### Objectives

Launching functional study of Chinese cabbage genes, whose function is not known, in *Arabidopsis*

### Materials and Methods

#### 1. Material

Plant - *Brassica rapa* ssp. *pekinensis* (Chiifu inbred, reference line of Chinese cabbage for The Multinational Brassica Genome Project)

EST (Expressed Sequence Tag)

#### 2. Methods:

A high-density colony array study (HDCA) was a choice of methods. We generated 10 high-density filters using Q-bot and hybridized with probes prepared using RNAs extracted from various stress-treated Chinese cabbage leaves.

### Results and Discussion

We have selected 4,195 clones, whose sequence homologs are not found in *Arabidopsis* genome and functions are largely unknown, from 100,041 ESTs (Expressed Sequence Tag) generated by over 20 cDNA libraries of *Brassica rapa* ssp. *pekinensis* (Chiifu inbred, reference line of Chinese cabbage for The Multinational Brassica Genome Project). This number occupies 11% of Chinese cabbage genes. To elucidate their function, we are planing to introduce them into *Arabidopsis* and examining their phenotypes.